



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/S17,707

Source:

PCT

Date Processed by STIC:

12-22-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/517/707

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading!)
 (xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING DATE: 12/22/2004
 PATENT APPLICATION: US/10/517,707 TIME: 16:16:10

Input Set : A:\MER134SEQLIST.TXT
 Output Set: N:\CRF4\12222004\J517707.raw

4 <110> APPLICANT: BAKER, Matthew
 5 CARR, Francis J.
 7 <120> TITLE OF INVENTION: MODIFIED BRYODIN 1 WITH REDUCED
 8 IMMUNOGENICITY
 10 <130> FILE REFERENCE: MER-134
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/517,707
 C--> 12 <141> CURRENT FILING DATE: 2004-12-10
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP03/06055
 13 <151> PRIOR FILING DATE: 2003-06-10
 15 <150> PRIOR APPLICATION NUMBER: EP 02012911.0
 16 <151> PRIOR FILING DATE: 2002-06-11
 18 <160> NUMBER OF SEQ ID NOS: 183
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 267
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
 28 Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Thr Thr Ser Tyr Gly Val
 29 1 5 10 15
 30 Phe Ile Lys Asn Leu Arg Glu Ala Leu Pro Tyr Glu Arg Lys Val Tyr
 31 20 25 30
 32 Asn Ile Pro Leu Leu Arg Ser Ser Ile Ser Gly Ser Gly Arg Tyr Thr
 33 35 40 45
 34 Leu Leu His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser Val Ala Val
 35 50 55 60
 36 Asp Val Thr Asn Val Tyr Ile Met Gly Tyr Leu Ala Gly Asp Val Ser
 37 65 70 75 80
 38 Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Phe Val Phe
 39 85 90 95
 40 Lys Asp Ala Lys Lys Lys Val Thr Leu Pro Tyr Ser Gly Asn Tyr Glu
 41 100 105 110
 42 Arg Leu Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu Gly
 43 115 120 125
 44 Leu Pro Ala Leu Asp Ser Ala Ile Thr Thr Leu Tyr Tyr Tyr Thr Ala
 45 130 135 140
 46 Ser Ser Ala Ala Ser Ala Leu Leu Val Leu Ile Gln Ser Thr Ala Glu
 47 145 150 155 160
 48 Ser Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val Asp
 49 165 170 175
 50 Lys Thr Phe Leu Pro Ser Leu Ala Thr Ile Ser Leu Glu Asn Asn Trp
 51 180 185 190
 52 Ser Ala Leu Ser Lys Gln Ile Gln Ile Ala Ser Thr Asn Asn Gly Gln

Does Not Comply
 Corrected Diskette Needed
 (PS.3-4)

RAW SEQUENCE LISTING

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DATE: 12/22/2004

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Input Set : A:\MER134SEQLIST.TXT

Output Set: N:\CRF4\12222004\J517707.raw

```

53          195          200          205
54 Phe Glu Ser Pro Val Val Leu Ile Asp Gly Asn Asn Gln Arg Val Ser
55          210          215          220
56 Ile Thr Asn Ala Ser Ala Arg Val Val Thr Ser Asn Ile Ala Leu Leu
57 225          230          235          240
58 Leu Asn Arg Asn Asn Ile Ala Ala Ile Gly Glu Asp Ile Ser Met Thr
59          245          250          255
60 Leu Ile Gly Phe Glu His Gly Leu Tyr Gly Ile
61          260          265
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 21
66 <212> TYPE: PRT
67 <213> ORGANISM: Homo sapiens
69 <400> SEQUENCE: 2
70 Arg Tyr Thr Leu Leu His Leu Thr Asn Tyr Ala Asp Glu Thr Ile Ser
71 1          5          10          15
72 Val Ala Val Asp Val
73          20
76 <210> SEQ ID NO: 3
77 <211> LENGTH: 15
78 <212> TYPE: PRT
79 <213> ORGANISM: Homo sapiens
81 <400> SEQUENCE: 3
82 Ala Thr Glu Ala Ala Lys Phe Val Phe Lys Asp Ala Lys Lys Lys
83 1          5          10          15
86 <210> SEQ ID NO: 4
87 <211> LENGTH: 24
88 <212> TYPE: PRT
89 <213> ORGANISM: Homo sapiens
91 <400> SEQUENCE: 4
92 Glu Arg Leu Gln Thr Ala Ala Gly Lys Ile Arg Glu Asn Ile Pro Leu
93 1          5          10          15
94 Gly Leu Pro Ala Leu Asp Ser Ala
95          20
98 <210> SEQ ID NO: 5
99 <211> LENGTH: 27
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 5
104 Ile Thr Thr Leu Tyr Tyr Tyr Thr Ala Ser Ser Ala Ala Ser Ala Leu
105 1          5          10          15
106 Leu Val Leu Ile Gln Ser Thr Ala Glu Ser Ala
107          20          25
110 <210> SEQ ID NO: 6
111 <211> LENGTH: 21
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 6
116 Ala Thr Ile Ser Leu Glu Asn Asn Trp Ser Ala Leu Ser Lys Gln Ile

```

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Input Set : A:\MER134SEQLIST.TXT

Output Set: N:\CRF4\12222004\J517707.raw

117 1 5 10 15
118 Gln Ile Ala Ser Thr
119 20
122 <210> SEQ ID NO: 7
123 <211> LENGTH: 268
124 <212> TYPE: PRT
125 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Modified byrocin 1 protein
W--> 130 <221> **VARIANT**
131 <222> LOCATION: 49, 50, 52, 55
132 <223> OTHER INFORMATION: Xaa=Ala, Gly, Pro
133 Xaa=Met, Ala, Gly, Pro, Ile
134 Xaa=Ala, Gly, Pro
135 Xaa=Pro, Tyr
W--> 137 <221> **VARIANT**
138 <222> LOCATION: 56, 61, 65, 67
139 <223> OTHER INFORMATION: Xaa=Thr, Ser
140 Xaa=Pro
141 Xaa=Ala, Gly, Pro
142 Xaa=Ala, Gly, Pro
W--> 144 <221> **VARIANT**
145 <222> LOCATION: 95, 96, 104
146 <223> OTHER INFORMATION: Xaa=Ala, Gly, Pro, His, Asp, Glu, Asn, Gln, Lys,
147 Arg, Ser, Thr
148 Xaa=Ala, Gly, Pro
149 Xaa=Ala, Gly, Pro
W--> 151 <221> **VARIANT**
152 <222> LOCATION: 115, 118, 120, 121
153 <223> OTHER INFORMATION: Xaa=Ala, Pro, Ser, Thr, His, Lys
154 Xaa=Thr
155 Xaa=His
156 Xaa=Ser
W--> 158 <221> **VARIANT**
159 <222> LOCATION: 122, 123, 126
160 <223> OTHER INFORMATION: Xaa=Ala, Ser, thr, Pro, Asn, Asp, Glu, Gly, His,
161 Lys, Gln
162 Xaa=Thr
163 Xaa=Ala, Pro
W--> 165 <221> **VARIANT**
166 <222> LOCATION: 130, 133, 137, 140
167 <223> OTHER INFORMATION: Xaa=Ala, Ile, Phe, Gly, Met, Pro, Val, Trp, Tyr
168 Xaa=Phe, Pro, Trp
169 Xaa=Ala, Gly, Pro
170 Xaa=Ala, Gly, Pro
W--> 173 <221> **VARIANT**
174 <222> LOCATION: 142, 143, 152, 153
175 <223> OTHER INFORMATION: Xaa=Ala, Gly, Pro
176 Xaa=Ala, Gly, Pro

What about location 1? 2
See ps. 4

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Input Set : A:\MER134SEQLIST.TXT

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177 Xaa=Ala, Gly, Pro, Ser, Thr
 178 Xaa=Ala, Gly, Pro, Ile, Met, Ser, Thr
 W--> 180 <221> VARIANT
 181 <222> LOCATION: 154, 155
 182 <223> OTHER INFORMATION: Xaa=Ala, Gly, Pro
 183 Xaa=Ala, Gly, Pro, Ser, Thr, His, Asp, Asn, Gln,
 184 Lys, Arg
 W--> 186 <221> VARIANT
 187 <222> LOCATION: 187, 189
 188 <223> OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
 189 Glu, Asn, Gln
 190 Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
 191 Glu, Asn, Gln
 W--> 193 <221> VARIANT
 194 <222> LOCATION: 196, 198
 195 <223> OTHER INFORMATION: Xaa=Gln
 196 Xaa=His, Lys, Arg, Asp, Glu, Asn,, Phe, Leu, Pro,
 197 Ser, Tyr, Trp
 W--> 199 <221> VARIANT
 200 <222> LOCATION: 200, 202
 201 <223> OTHER INFORMATION: Xaa=Ala, Gly, Pro, Thr, Ser, His, Lys, Arg, Asp,
 202 Glu, Asn, Gln
 203 Xaa=Asp
 W--> 205 <400> 7
 W--> 206 (Xaa) Asp Val Ser Phe Arg Leu Ser Gly Ala Thr Thr Thr Ser Tyr Gly
 207 1 5 10 15
 208 Val Phe Ile Lys Asn Leu Arg Glu Ala Leu Pro Tyr Glu Arg Lys Val
 209 20 25 30
 210 Tyr Asn Ile Pro Leu Leu Arg Ser Ser Ile Ser Gly Ser Gly Arg Tyr
 211 35 40 45
 212 Xaa Xaa Leu Xaa Leu Thr Xaa Xaa Ala Asp Glu Thr Xaa Ser Val Ala
 213 50 55 60
 214 Xaa Asp Xaa Thr Asn Val Tyr Ile Met Gly Tyr Leu Ala Gly Asp Val
 215 65 70 75 80
 216 Ser Tyr Phe Phe Asn Glu Ala Ser Ala Thr Glu Ala Ala Lys Xaa Xaa
 217 85 90 95
 218 Phe Lys Asp Ala Lys Lys Lys Xaa Thr Leu Pro Tyr Ser Gly Asn Tyr
 219 100 105 110
 220 Glu Arg Xaa Gln Thr Xaa Ala Xaa Xaa Xaa Xaa Glu Asn Xaa Pro Leu
 221 115 120 125
 222 Gly Xaa Pro Ala Xaa Asp Ser Ala Xaa Thr Thr Xaa Tyr Xaa Xaa Thr
 223 130 135 140
 224 Ala Ser Ser Ala Ala Ser Ala Xaa Xaa Xaa Xaa Ile Gln Ser Thr Ala
 225 145 150 155 160
 226 Glu Ser Ala Arg Tyr Lys Phe Ile Glu Gln Gln Ile Gly Lys Arg Val
 227 165 170 175
 228 Asp Lys Thr Phe Leu Pro Ser Leu Ala Thr Xaa Ser Xaa Glu Asn Asn
 229 180 185 190
 230 Trp Ser Ala Xaa Ser Xaa Gln Xaa Gln Xaa Ala Ser Thr Asn Asn Gly

See item # 9 on error summary sheet.

pls explain "Xaa" location

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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Input Set : A:\MER134SEQLIST.TXT

Output Set: N:\CRF4\12222004\J517707.raw

```

231          195          200          205
232 Gln Phe Glu Ser Pro Val Val Leu Ile Asp Gly Asn Asn Gln Arg Val
233          210          215          220
234 Ser Ile Thr Asn Ala Ser Ala Arg Val Val Thr Ser Asn Ile Ala Leu
235 225          230          235          240
236 Leu Leu Asn Arg Asn Asn Ile Ala Ala Ile Gly Glu Asp Ile Ser Met
237          245          250          255
238 Thr Leu Ile Gly Phe Glu His Gly Leu Tyr Gly Ile
239          260          265
242 <210> SEQ ID NO: 8
243 <211> LENGTH: 13
244 <212> TYPE: PRT
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Flu protein fragment
250 <400> SEQUENCE: 8
251 Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
252 1          5          10
255 <210> SEQ ID NO: 9
256 <211> LENGTH: 15
257 <212> TYPE: PRT
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Chlamydia peptide
263 <400> SEQUENCE: 9
264 Lys Val Val Asp Gln Ile Lys Lys Ile Ser Lys Pro Val Gln His
265 1          5          10          15
268 <210> SEQ ID NO: 10
269 <211> LENGTH: 13
270 <212> TYPE: PRT
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Fragments of Bryodin 1
276 <400> SEQUENCE: 10
277 Val Ser Phe Arg Leu Ser Gly Ala Thr Thr Thr Ser Tyr
278 1          5          10
281 <210> SEQ ID NO: 11
282 <211> LENGTH: 13
283 <212> TYPE: PRT
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Fragments of Bryodin 1
289 <400> SEQUENCE: 11
290 Phe Arg Leu Ser Gly Ala Thr Thr Thr Ser Tyr Gly Val
291 1          5          10
294 <210> SEQ ID NO: 12
295 <211> LENGTH: 13
296 <212> TYPE: PRT
297 <213> ORGANISM: Artificial Sequence

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/517,707

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TIME: 16:16:11

Input Set : A:\MER134SEQLIST.TXT
Output Set: N:\CRF4\12222004\J517707.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 1, 48, 50, 52, 55, 56, 61, 65, 67, 95, 96, 104, 115, 118, 120, 121, 122

Seq#:7; Xaa Pos. 123, 126, 130, 133, 137, 140, 142, 143, 152, 153, 154, 155, 167, 189

Seq#:7; Xaa Pos. 195, 198, 200, 202

VERIFICATION SUMMARY

DATE: 12/22/2004

PATENT APPLICATION: US/10/517,707

TIME: 16:16:11

Input Set : A:\MER134SEQLIST.TXT

Output Set: N:\CRF4\12222004\J517707.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:130 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:137 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:144 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:151 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:158 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:165 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:173 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:180 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:186 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:193 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:199 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:205 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
M:341 Repeated in SeqNo=7